

Db 168 GCTGAAATACGCCAGCAAATCCCCGTTTTTAGACAGAAGCGATCAGACCTCTATGCTGTG 109

Qy 814 GAGATGAAAAAGCCCTAA 831

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Db 108 GAGATGAAAAAGCCCTAA 91

SEQ ID NO:2, Standard, AA database

Q9NQR4

ID Q9NQR4 PRELIMINARY; PRT; 276 AA.
AC Q9NQR4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE NIT protein 2 (CUA002).
GN NIT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=10959838;
RA Pace H.C., Hodawadekar S.C., Draganescu A., Huang J., Bieganowski P.,
RA Pekarisky Y., Croce C.M., Brenner C.;
RT "Crystal structure of the worm NitFhit Rosetta Stone protein reveals a
RT Nit tetramer binding two Fhit dimers."
RL Curr. Biol. 10:907-917(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=ADRENOCORTICAL TUMOR SECRETED ACTH;
RA Xu X., Yang Y., Gao G., Xiao H., Chen Z., Han Z.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF284574; AAF87103.1; -.
DR EMBL; AF260334; AAG44665.1; -.
DR InterPro; IPR003010; Ntlse/CNhydtse.
DR Pfam; PF00795; CN_hydrolase; 1.
SQ SEQUENCE 276 AA; 30608 MW; 32FA797601A419C6 CRC64;

Query Match 100.0%; Score 1438; DB 4; Length 276;
Best Local Similarity 100.0%; Pred. No. 1.6e-124;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	121	PGKITFQESKTLSPGDSFSTFDTPYCRVGLGICYDMRFAELAQIYAQRGCQLLVYPGAFN	180
Qy	181	LTTGPAHWELLQRSRAVDNQVYVATASPARDDKASYVAWGHSTVVNPWGEVLAKAGTEEA	240
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Db	241	IVYSDIDLKKLAEIRQQIPVFRQKRSPLYAVEMKKP	276

SEQ ID NO:2, Standard
AF284574
LOCUS AF284574 962 bp mRNA linear PRI 24-JUL-2000
DEFINITION Homo sapiens Nit protein 2 (NIT2) mRNA, complete cds.
ACCESSION AF284574
VERSION AF284574.1 GI:9367115
KEYWORDS .
SOURCE Homo sapiens.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 962)
AUTHORS Pace,H.C., Hodawadekar,S.C., Draganescu,A., Huang,J.,
Bieganski,P., Pekarsky,Y., Croce,C.M. and Brenner,C.
TITLE Crystal structure of the worm NitFhit Rosetta Stone protein reveals
a Nit tetramer binding two Fhit dimers
JOURNAL Curr. Biol. 10 (15), 907-917 (2000)
MEDLINE 20414396
PUBMED 10959838

REFERENCE 2 (bases 1 to 962)
AUTHORS Pace,H.C., Hodawadekar,S.C., Draganescu,A., Huang,J.,
Bieganski,P., Pekarsky,Y., Croce,C.M. and Brenner,C.
TITLE Direct Submission
JOURNAL Submitted (05-JUL-2000) Kimmel Cancer Center, Thomas Jefferson
University, 233 S 10th Street, Rm. 826, Philadelphia, PA 19107, USA

FEATURES Location/Qualifiers
source 1..962
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gene 1..962
/gene="NIT2"
CDS 22..852
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elegans NitFhit and Drosophila melanogaster NitFhit"
/codon_start=1
/product="Nit protein 2"
/protein_id="AAF87103.1"
/db_xref="GI:9367116"
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LAQIYAQRGCQLLVYPGAFNLTGPAHWELLQRSRAVDNQVYVATASPARDDKASYVA
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BASE COUNT 283 a 208 c 218 g 253 t
ORIGIN

Alignment Scores:

Pred. No.:	1.37e-137	Length:	962
Score:	1438.00	Matches:	276
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-769-952-2 (1-276) x AF284574 (1-962)

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Db	82	GTCACCTCGCGCTTGTAGCTTCATCCGGGAGGCAACGCAAGGAGCCAAATAGTTTCT	141
QY	41	LeuProGluCysPheAsnSerProTyrGlyAlaLysTyrPheProGluTyrAlaGluLys	60
Db	142	TTGCCGAATGCTTTAATTCTCCATATGGAGCGAAATATTTCTGAATATGCAGAGAAA	201
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Db	262		ATTGGAGGCTCTATCCCTGAAGAGGATGCTGGGAAATTATATAACACCTGTGCTGTGTTT	321
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Db	382		CCTGGAAAAATTACATTTCAAGAATCTAAACATTGAGTCCGGGTGATAGTTTCTCCACA	441
Qy	141		PheAspThrProTyrCysArgValGlyLeuGlyIleCysTyrAspMetArgPheAlaGlu	160
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Db	502		CTTGCAAAATCTACGCACAGAGAGGCTGCCAGCTGTTGGTATATCCAGGAGCTTTTAAT	561
Qy	181		LeuThrThrGlyProAlaHisTrpGluLeuLeuGlnArgSerArgAlaValAspAsnGln	200
Db	562		CTGACCACTGGACCAGCCATTGGGAGTTACTTCAGCGAAGCCGGGCTGTTGATAATCAG	621
Qy	201		ValTyrValAlaThrAlaSerProAlaArgAspAspLysAlaSerTyrValAlaTrpGly	220
Db	622		GTGTATGTGGCCACAGCCTCTCCTGCCCGGGATGACAAAGCCTCCTATGTTGCCTGGGGA	681
Qy	221		HisSerThrValValAsnProTrpGlyGluValLeuAlaLysAlaGlyThrGluGluAla	240
Db	682		CACAGCACCGTGGTGAACCCTTGGGGGGAGGTTCTAGCCAAAGCTGGCACAGAAGAAGCA	741
Qy	241		IleValTyrSerAspIleAspLeuLysLysLeuAlaGluIleArgGlnGlnIleProVal	260
Db	742		ATCGTGATTTCAGACATAGACCTGAAGAAGCTGGCTGAAATACGCCAGCAATCCCCGTT	801
Qy	261		PheArgGlnLysArgSerAspLeuTyrAlaValGluMetLysLysPro	276
Db	802		TTTAGACAGAAGCGATCAGACCTCTATGCTGTGGAGATGAAAAGCCCC	849